

CALTE.015ASEQLIST.txt

SEQUENCE LISTING

<110> Anderson, David J.  
Dong, Xinzhong  
Zylka, Mark

<120> IDENTIFICATION OF A RECEPTOR CONTROLLING MIGRATION AND METASTASIS OF SKIN  
CANCER CELLS

<130> CALTE.0015A

<150> US 60/391,127

<151> 2000-06-21

<160> 4

<170> FastSEQ for windows Version 4.0

<210> 1

<211> 1361

<212> DNA

<213> Mus musculus

<220>

<221> CDS

<222> (48)...(1064)

<400> 1

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gtc atc caa gac tgg acc att aat att aca gca ctg aaa gaa agc aat 104
Val Ile Gln Asp Trp Thr Ile Asn Ile Thr Ala Leu Lys Glu Ser Asn
      5                      10                      15

gac aat gga ata tca ttt tgt gaa gtt gtg tct cgt acc atg act ttt 152
Asp Asn Gly Ile Ser Phe Cys Glu Val Val Ser Arg Thr Met Thr Phe
      20                      25                      30                      35

ctt tcc ctc atc att gcc tta gtt ggg ctg gtt gga aat gcc aca gtg 200
Leu Ser Leu Ile Ile Ala Leu Val Gly Leu Val Gly Asn Ala Thr Val
                        40                      45                      50

tta tgg ttt ctg ggc ttc cag atg agc agg aat gcc ttc tct gtc tac 248
Leu Trp Phe Leu Gly Phe Gln Met Ser Arg Asn Ala Phe Ser Val Tyr
                        55                      60                      65

atc ctc aac ctt gct ggt gct gac ttt gtc ttc atg tgc ttt caa att 296
Ile Leu Asn Leu Ala Gly Ala Asp Phe Val Phe Met Cys Phe Gln Ile
                        70                      75                      80

gta cat tgt ttt tat att atc tta gac atc tac ttc atc ccc act aat 344
Val His Cys Phe Tyr Ile Ile Leu Asp Ile Tyr Phe Ile Pro Thr Asn
      85                      90                      95

ttt ttt tca tct tac act atg gtg tta aac att gct tac ctt agt ggt 392
Phe Phe Ser Ser Tyr Thr Met Val Leu Asn Ile Ala Tyr Leu Ser Gly
      100                      105                      110                      115

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ctg agc atc ctc act gtc att agc act gaa cgc ttc cta tct gtc atg Leu Ser Ile Leu Thr Val Ile Ser Thr Glu Arg Phe Leu Ser Val Met 120 125 130	440
tgg ccc atc tgg tac cgc tgc caa cgc cca agg cac aca tca gct gtc Trp Pro Ile Trp Tyr Arg Cys Gln Arg Pro Arg His Thr Ser Ala Val 135 140 145	488
ata tgt act gtg ctt tgg gtc ttg tcc ctg gtg ttg agc ctc ctg gaa Ile Cys Thr Val Leu Trp Val Leu Ser Leu Val Leu Ser Leu Glu 150 155 160	536
gga aag gaa tgt ggc ttc cta tat tac act agt ggc cct ggt ttg tgt Gly Lys Glu Cys Gly Phe Leu Tyr Tyr Thr Ser Gly Pro Gly Leu Cys 165 170 175	584
aag aca ttt gat tta atc act act gca tgg tta att gtt tta ttt gtg Lys Thr Phe Asp Leu Ile Thr Thr Ala Trp Leu Ile Val Leu Phe Val 180 185 190 195	632
gtt ctc ttg gga tcc agt ctg gcc ttg gtg ctt acc atc ttc tgt ggc Val Leu Leu Gly Ser Ser Leu Ala Leu Val Leu Thr Ile Phe Cys Gly 200 205 210	680
tta cac aag gtt cct gtg acc agg ttg tat gtg acc att gtg ttt aca Leu His Lys Val Pro Val Thr Arg Leu Tyr Val Thr Ile Val Phe Thr 215 220 225	728
gtg ctt gtc ttc ctg atc ttt ggt ctg ccc tat ggg atc tac tgg ttc Val Leu Val Phe Leu Ile Phe Gly Leu Pro Tyr Gly Ile Tyr Trp Phe 230 235 240	776
ctc tta gag tgg att agg gaa ttt cat gat aat aaa cct tgt ggt ttt Leu Leu Glu Trp Ile Arg Glu Phe His Asp Asn Lys Pro Cys Gly Phe 245 250 255	824
cgt aac gtg aca ata ttt ctg tcc tgt att aac agc tgt gcc aac ccc Arg Asn Val Thr Ile Phe Leu Ser Cys Ile Asn Ser Cys Ala Asn Pro 260 265 270 275	872
atc att tac ttc ctt gtt ggc tcc att agg cac cat cgg ttt caa cgg Ile Ile Tyr Phe Leu Val Gly Ser Ile Arg His His Arg Phe Gln Arg 280 285 290	920
aag act ctc aag ctt ctt ctg cag aga gcc atg caa gac tct cct gag Lys Thr Leu Lys Leu Leu Leu Gln Arg Ala Met Gln Asp Ser Pro Glu 295 300 305	968
gag gaa gaa tgt gga gag atg ggt tcc tca aga aga cct aga gaa ata Glu Glu Glu Cys Gly Glu Met Gly Ser Ser Arg Arg Pro Arg Glu Ile 310 315 320	1016
aaa act gtc tgg aag gga ctg aga gct gct ttg atc agg cat aaa tag Lys Thr Val Trp Lys Gly Leu Arg Ala Ala Leu Ile Arg His Lys * 325 330 335	1064
ctttgaagag aactatgttt ttatcacttt gtggcatttt cataatgttg tttagttgat gacccaaggt taactcagtt ggggaagtag tcaatgttgt agaagttgat tgatattgaa cttgttataa atactgagta cagtattttt gcagctatct tgctcagagc tttaccaact ccatttgatg ggactcctta taagctctat ggggtccagg agaggtgttg accacaattg acaaatccct cttcagaaga aaactcaaga aagtgcattg aaaagttata tttctttt 1124 1184 1244 1304 1361	

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<211> 338  
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 <213> Mus musculus

<400> 2

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 20      25      30
Met Thr Phe Leu Ser Leu Ile Ile Ala Leu Val Gly Leu Val Gly Asn
 35      40      45
Ala Thr Val Leu Trp Phe Leu Gly Phe Gln Met Ser Arg Asn Ala Phe
 50      55      60
Ser Val Tyr Ile Leu Asn Leu Ala Gly Ala Asp Phe Val Phe Met Cys
 65      70      75      80
Phe Gln Ile Val His Cys Phe Tyr Ile Ile Leu Asp Ile Tyr Phe Ile
 85      90      95
Pro Thr Asn Phe Phe Ser Ser Tyr Thr Met Val Leu Asn Ile Ala Tyr
100      105      110
Leu Ser Gly Leu Ser Ile Leu Thr Val Ile Ser Thr Glu Arg Phe Leu
115      120      125
Ser Val Met Trp Pro Ile Trp Tyr Arg Cys Gln Arg Pro Arg His Thr
130      135      140
Ser Ala Val Ile Cys Thr Val Leu Trp Val Leu Ser Leu Val Leu Ser
145      150      155      160
Leu Leu Glu Gly Lys Glu Cys Gly Phe Leu Tyr Tyr Thr Ser Gly Pro
165      170      175
Gly Leu Cys Lys Thr Phe Asp Leu Ile Thr Thr Ala Trp Leu Ile Val
180      185      190
Leu Phe Val Val Leu Leu Gly Ser Ser Leu Ala Leu Val Leu Thr Ile
195      200      205
Phe Cys Gly Leu His Lys Val Pro Val Thr Arg Leu Tyr Val Thr Ile
210      215      220
Val Phe Thr Val Leu Val Phe Leu Ile Phe Gly Leu Pro Tyr Gly Ile
225      230      235      240
Tyr Trp Phe Leu Leu Glu Trp Ile Arg Glu Phe His Asp Asn Lys Pro
245      250      255
Cys Gly Phe Arg Asn Val Thr Ile Phe Leu Ser Cys Ile Asn Ser Cys
260      265      270
Ala Asn Pro Ile Ile Tyr Phe Leu Val Gly Ser Ile Arg His His Arg
275      280      285
Phe Gln Arg Lys Thr Leu Lys Leu Leu Leu Gln Arg Ala Met Gln Asp
290      295      300
Ser Pro Glu Glu Glu Glu Cys Gly Glu Met Gly Ser Ser Arg Arg Pro
305      310      315      320
Arg Glu Ile Lys Thr Val Trp Lys Gly Leu Arg Ala Ala Leu Ile Arg
325      330      335
His Lys
    
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<210> 3  
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 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> (171)...(1160)

<400> 3

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gctcaagtct tgtttttgtt tccaggggca ccagtggagg ttttctgagc atg gat 176
    
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Met Asp  
1

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tgg ttc cta ata tta tgg atc tgg aag gat tct gat gtc tta ttt tgt 944
Trp Phe Leu Ile Leu Trp Ile Trp Lys Asp Ser Asp Val Leu Phe Cys
245 250 255

cat att cat cca gtt tca gtt gtc ctg tca tct ctt aac agc agt gcc 992
His Ile His Pro Val Ser Val Val Leu Ser Ser Leu Asn Ser Ser Ala
260 265 270

aac ccc atc att tac ttc ttc gtg ggc tct ttt agg aag cag tgg cgg 1040
Asn Pro Ile Ile Tyr Phe Phe Val Gly Ser Phe Arg Lys Gln Trp Arg
275 280 285

ctg cag cag ccg atc ctc aag ctg gct ctc cag agg gct ctg cag gac 1088
Leu Gln Gln Pro Ile Leu Lys Leu Ala Leu Gln Arg Ala Leu Gln Asp
295 300 305

att gct gag gtg gat cac agt gaa gga tgc ttc cgt cag ggc acc ccg 1136
Ile Ala Glu Val Asp His Ser Glu Gly Cys Phe Arg Gln Gly Thr Pro
310 315 320

gag atg tcg aga agc agt ctg gtg tagagatgga cagcctctac ttccatcaga 1190
Glu Met Ser Arg Ser Ser Leu Val
325 330

tatatgtggc tttgagaggc aactttgccc ctgtctgtct gatttgctga actttctcag 1250
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 <211> 330  
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Pro Val Phe Leu Ile Leu Phe Ile Ala Leu Val Gly Leu Val Gly Asn
35 40 45
Gly Phe Val Leu Trp Leu Leu Gly Phe Arg Met Arg Arg Asn Ala Phe
50 55 60
Ser Val Tyr Val Leu Ser Leu Ala Gly Ala Asp Phe Leu Phe Leu Cys
65 70 75 80
Phe Gln Ile Ile Asn Cys Leu Val Tyr Leu Ser Asn Phe Phe Cys Ser
85 90 95
Ile Ser Ile Asn Phe Pro Ser Phe Phe Thr Thr Val Met Thr Cys Ala
100 105 110
Tyr Leu Ala Gly Leu Ser Met Leu Ser Thr Val Ser Thr Glu Arg Cys
115 120 125
Leu Ser Val Leu Trp Pro Ile Trp Tyr Arg Cys Arg Arg Pro Arg His
130 135 140
Leu Ser Ala Val Val Cys Val Leu Leu Trp Ala Leu Ser Leu Leu Leu
145 150 155 160
Ser Ile Leu Glu Gly Lys Phe Cys Gly Phe Leu Phe Ser Asp Gly Asp
165 170 175
Ser Gly Trp Cys Gln Thr Phe Asp Phe Ile Thr Ala Ala Trp Leu Ile
180 185 190
Phe Leu Phe Met Val Leu Cys Gly Ser Ser Leu Ala Leu Leu Val Arg
195 200 205
Ile Leu Cys Gly Ser Arg Gly Leu Pro Leu Thr Arg Leu Tyr Leu Thr
210 215 220
Ile Leu Leu Thr Val Leu Val Phe Leu Leu Cys Gly Leu Pro Phe Gly
225 230 235 240

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CALTE.015ASEQLIST.txt

Ile	Gln	Trp	Phe	Leu	Ile	Leu	Trp	Ile	Trp	Lys	Asp	Ser	Asp	Val	Leu
				245					250					255	
Phe	Cys	His	Ile	His	Pro	Val	Ser	Val	Val	Leu	Ser	Ser	Leu	Asn	Ser
			260					265					270		
Ser	Ala	Asn	Pro	Ile	Ile	Tyr	Phe	Phe	Val	Gly	Ser	Phe	Arg	Lys	Gln
		275					280					285			
Trp	Arg	Leu	Gln	Gln	Pro	Ile	Leu	Lys	Leu	Ala	Leu	Gln	Arg	Ala	Leu
	290					295					300				
Gln	Asp	Ile	Ala	Glu	Val	Asp	His	Ser	Glu	Gly	Cys	Phe	Arg	Gln	Gly
305					310					315					320
Thr	Pro	Glu	Met	Ser	Arg	Ser	Ser	Leu	Val						
				325					330						